# New altitudinal record of *Myotis moratellii* Novaes et al., 2021 (Chiroptera, Vespertilionidae) in the northwestern foothills of Ecuador

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**Abstract.** *Myotis moratellii* Novaes et al., 2021 is a bat species that inhabits western Ecuador at low elevations (0–150 m a.s.l.). This study extends its northern distribution by 63 km into the foothill rainforests of the Chocó in Imbabura Province at 1,240 m a.s.l. Given the novel color patterns observed in the specimens collected, molecular approaches were necessary for species-level identification. Although the cause of this variation remains unclear, continued integrative taxonomy is critical to uncover the cryptic diversity within the genus.

**Key words.** Chocó, color variation, cryptic diversity, cytochrome b, distribution, elevation, premontane forest

## INTRODUCTION

Bats are one of Ecuador's most studied orders of mammals (see Albuja 1982, 1999; Albuja and Mena 2004; Larsen et al. 2012; Tirira 2017; Carrión-Bonilla et al. 2024). To date, 182 species of bats have been recorded in the country (Tirira et al. 2024). The knowledge of bat diversity in Ecuador has improved recently through taxonomic revisions integrating morphological and molecular data to identify previously unrecognized species within cryptic complexes (see Novaes et al. 2021; Yánez-Fernández et al. 2023; Camacho et al. 2024).

This is particularly evident in *Myotis* Kaup, 1829, the most diverse genus of bats comprising 139 recognized species in the world (Simmons and Cirranello 2025). In Ecuador, 10 species have been reported (Carrión-Bonilla and Cook 2020; Novaes et al. 2021; Carrión-Bonilla et al. 2024), including cryptic species complexes such as *M. riparius* Handley, 1960 (Novaes et al. 2024) and *M. keaysi* J.A. Allen, 1914 (Novaes et al. 2021). In the last decade, increased surveys efforts in museums and surveys in previously unexplored geographic regions (Moratelli et al. 2011, 2013; Moratelli and Wilson 2015; Carrión-Bonilla et al. 2024), coupled with integrative taxonomy (Novaes et al. 2024) and the analysis of Ultraconserved Elements (Korstian et al. 2024), have shed light on the evolutionary relationships of this rapid radiation of bats.

These efforts have led to the description of new species, including one from the *M. keaysi* complex inhabiting the western coast of Ecuador (Novaes et al. 2021). *Myotis moratellii* Novaes et al., 2021 is a medium-sized species in the ruber group (Novaes et al. 2021), which has records from the provinces of El Oro, Los Ríos, and Esmeraldas, yet its habitat has been restricted to the tropical monsoon ecoregion in seasonal dry forests of the Chocó and tropical broadleaf dry forests at maximum altitudes of 150 m a.s.l. (Novaes et al. 2021). However, these geographic and ecological boundaries are sometimes an artifact of limited sampling of poorly known species as demonstrated for other Neotropical *Myotis* by Carrión-Bonilla et al. (2024). The northwestern region in Ecuador, for example, is typically overlooked due to its challenging topographic and logistical complexities (Brito et al. 2020). As a result, local species composition and genetic variation remain unknown and further complicated by cryptic species complexes for which species-level identification via morphologic analysis can be unreliable (Korstian et al. 2024).

Here, we document a new altitudinal record for *M. moratellii* in the Reserva Río Manduriacu, which also extends its northern distribution in Ecuador.

## METHODS

**Collection and study of specimens.** One sampling campaign was carried out in May 2024 in the Reserva Río Manduriacu in the Chocó ecoregion, in northwestern Ecuador. Sampling was carried out for 6 nights, using 8 mist nets of 6, 10 and 12 m (Kurta and Kunz 1988). The nets remained open between 18:30 and 21:30 pm with a total effort of 1,296 m/18 h (Medellin 1993). Standard external body measurements (mm) were taken post-mortem from each individual (total length, tail length, right forearm, right ear length, right tragus, weight (g)), as well as the sex and reproductive status. Cranial measurements of collected specimens were taken with digital calipers of precision of 0.1 mm. Body and cranial measurements, as well as other species-specific characteristics follow Novaes et al. (2021). To make fur color comparable to other studies, we followed the standardized color nomenclature of Ridgway (1912). Voucher specimens were deposited in the Instituto Nacional de Biodiversidad (INABIO), formerly, Museo Ecuatoriano de Ciencias Naturales (MECN), Quito, Ecuador. We preserved MECN 8004 as skin, skull, and skeleton, and MECN 8096 in 10% formalin.

The study was conducted under collection permit no. MAATE-ARSFC-2023-0145, and authorization of access to genetic resources no. MAATE-DBI-CM-2023-0334, both issued by the Ministerio del Ambiente, Agua y Transición Ecológica de Ecuador. Collecting of the specimens was made following the ethical guidelines of the American Society of Mammalogists (Sikes et al. 2016).

**DNA extraction, sequence generation and assembly.** To obtain sequence data, DNA was isolated from the liver using the GeneJET Genomic DNA Purification Kit (K0722). The amplification process of the full-length mitochondrial cytochrome b (Cytb) gene was achieved via Polymerase Chain Reaction (PCR) with the forward and reverse primers MVZ05 and MVZ16 (Smith and Patton 1993), and the GoTaq® Green Master Mix 2X kit. The PCR protocol included an initial denaturation step at 95 °C for 2 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 45 °C for 30 s, and extension at 72 °C for 80 s, concluding with a final extension at 72 °C for 5 min, modified from Hurtado and Pacheco (2017). Sequencing of the Cytb was conducted using a MinION mk1c equipped with Flongle Flow Cells R10.4.1 and the Rapid Barcoding Kit 96 (SQK-RBK114.96), adhering to standard protocols. Data were basecalled with Dorado v. 0.5.2 and the high accuracy model v. 4.3.0., to obtain good quality sequences for phylogenetic analysis (Sanderson et al. 2024). The resulting fastq files were filtered at a Q score of 9, and consensus sequences were generated using NGSpecies ID v. 0.3.0 (Sahlin et al. 2021). DNA extraction, PCR amplification and sequencing with Oxford Nanopore Technologies were performed at the Nucleic Acid Sequencing Laboratory of the INABIO in Quito, Ecuador.

**Phylogenetics analyses and genetic distances.** To provide phylogenetic context, we downloaded Cytb sequences from NCBI for all species described to date in the ruber group (Carrión-Bonilla and Cook 2020; Novaes et al. 2021; Carrión-Bonilla et al. 2024), and three species from the albescens group as the outgroup (Table 1A). The multiple sequence alignment (MSA) of 69 Cytb sequences was generated with the online MAFFT tool v. 7 with default settings, and resulted in an alignment containing 48 constant sites, 297 parsimony informative sites, and 374 distinct site patterns.

To assess assumptions of homogeneity and stationarity we tested three maximal matched-pair tests of symmetry (Naser-Khdour et al. 2019) in the MSA prior to phylogenetic analysis in IQ-TREE 2 v. 2.3.0 (Minh et al. 2020). Subsequently, the nucleotide substitution model for codon positions was estimated using ModelFinder (Kalyaanamoorthy et al. 2017) and selected via the Bayesian Information Criterion within the IQ-TREE 2 pipeline. The reconstruction of phylogenetic relationships using Maximum Likelihood (ML) was conducted with the best-fit Muse-Gaut model (Muse and Gaut 1994) with unequal nucleotide frequencies and four gamma categories (MG+F3X4+G4), selecting *Myotis levis* I. Geoffroy Saint-Hilaire, 1824 as the outgroup taxon to root the tree. Nodal supports were calculated with the UltraFast Bootstrap approximation (UF; Minh et al. 2013) to reduce the impact of severe model violations, and the SH-approximate likelihood ratio test (SH; Guindon et al. 2010) with 1,000 bootstrap replicates.

To validate species identities, we employed the phylogenetic species concept (De Queiroz 2007) and considered a highly supported clade (UF ≥ 95 and SH ≥ 80, Minh et al. 2013) to represent a single evolutionary unit. Additionally, we used the genetic species concept as a predictor of species limits (Baker and Bradley 2006). We set a threshold of 3% as a measure of intraspecific genetic variation, and greater than 3% to delimit sister taxa as empirically seen for *Myotis* (see Baker and Bradley 2006 and references therein). To model genetic distances, we used MEGA v. 11.0.13 (Tamura et al. 2021). We first calculated the gamma parameter with the ML Estimate Rate Variation among Sites tool with four discrete categories and a moderate branch swap filter and then computed within and between-group divergence values with the Kimura 2-parameter model (Kimura 1981).

# RESULTS

***Myotis moratellii* Novaes, Cláudio, Carrión-Bonilla, Abreu, Wilson, Maldonado & Weksler, 2021**
Figures 1–3

**New record.** ECUADOR — Imbabura • Cotacachi, García Moreno, Reserva Río Manduriacu; 00.3104, −078.8578; 1,240 m alt.; 18.V.2024; F.X. Castellanos, L. Simba and J. Brito leg.; GenBank PV106025 and PV106026; 2 ♂, MECN 8004 (JBM 3257) and MECN 8096 (JBM 3279).

**Identification.** According to Novaes et al. (2021), *M. moratellii* is of medium size (forearm length 35–38.2 mm; total length 76–89 mm; greatest length of skull 13.79–14.05 mm). However, the specimens from Imbabura have slightly larger forearms but similar total length (Table 1). Ears are comparatively short with elongated tragus and the tip rounded (Figure 1).

The pelage of *M. moratellii* is woolly and moderately long with Buckthorn Brown unicolored dorsal hairs as in MECN 8004 (Figures 1A, 2); upper dorsum of uropatagium covered with Dresden Brown hair extending to just beyond the knees; plagiopatagium attached to the foot by a broad band of membrane (Figure 2), and an absent fringe of hairs on the distal border of the uropatagium. Central part of the abdomen Mummy Brown, with Ochraceous-Orange sides (Figure 2B). Conversely the ventral fur of MECN 8096 is Mummy Brown with a ventral and pectoral patch of Maize Yellow and Ochraceous-Orange hairs; the dorsal fur is Dresden Brown with lighter dispersed patches of Ochraceous-Orange hairs from the base of the tail towards the skull and rostrum (Figure 1B).

The skull of MECN 8004 is similar to the holotype (Table 1). Medium sagittal crest present; skull robust and broad; braincase inflated and noticeably high in profile; roof of the braincase formed by the parietal bone subtly sloping forward; frontal bone steeply sloping in lateral view; posterior region of the braincase rounded and projecting beyond the boundary of the occipital condyles; mastoid processes well developed (Figure 3).

**Molecular analysis.** The ML phylogenetic tree shows MECN 8004 and MECN 8096 nested in a highly supported clade with representatives of *M. moratellii* from the provinces of El Oro and Los Ríos (Figure 4A;

**Figure 1.** Fronto-lateral view of two live *Myotis moratellii* captured in the Reserva Río Manduriacu. **A.** MECN 8004. **B.** MECN 8096. Photos by Jorge Brito.
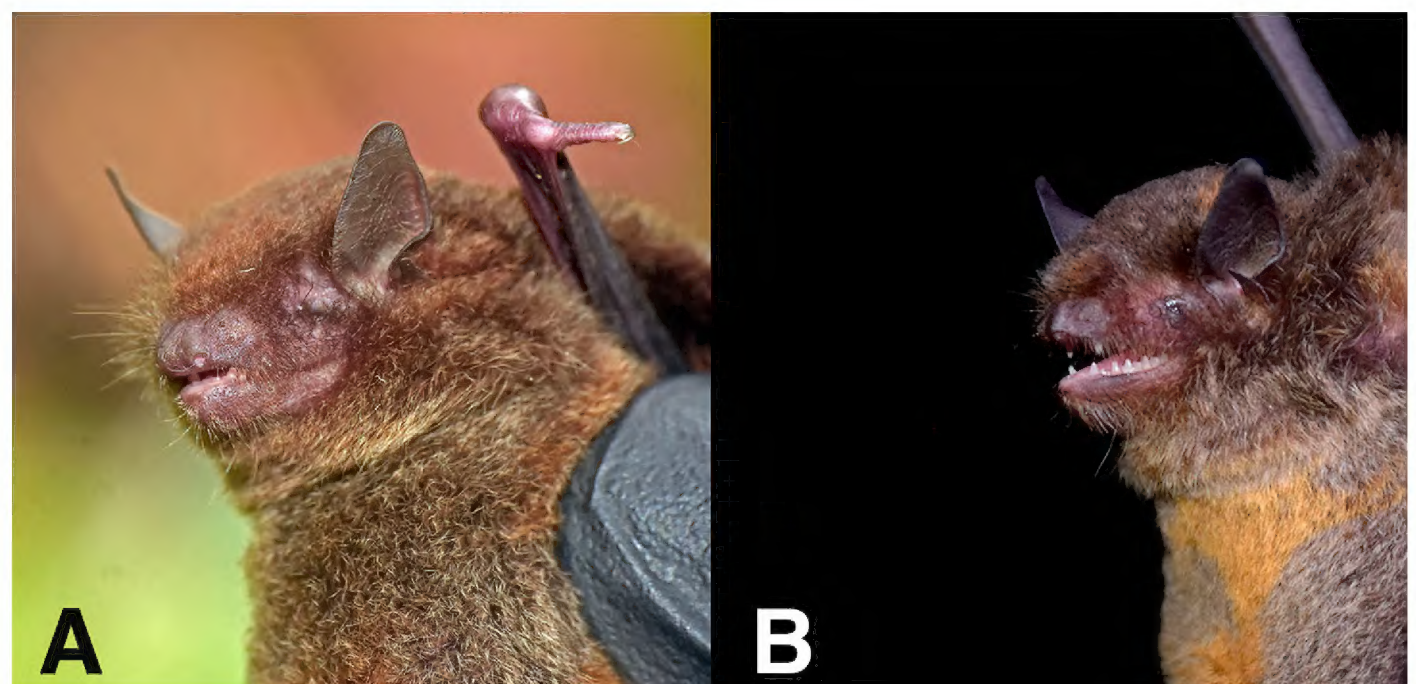


**Figure 2.** Whole body view of *Myotis moratellii* (MECN 8004) post-mortem. **A.** Dorsal view. **B.** Ventral view. Note Ochraceous-Orange patches of fur in both views. Scale bar = 5 mm. Photos by Jorge Brito.
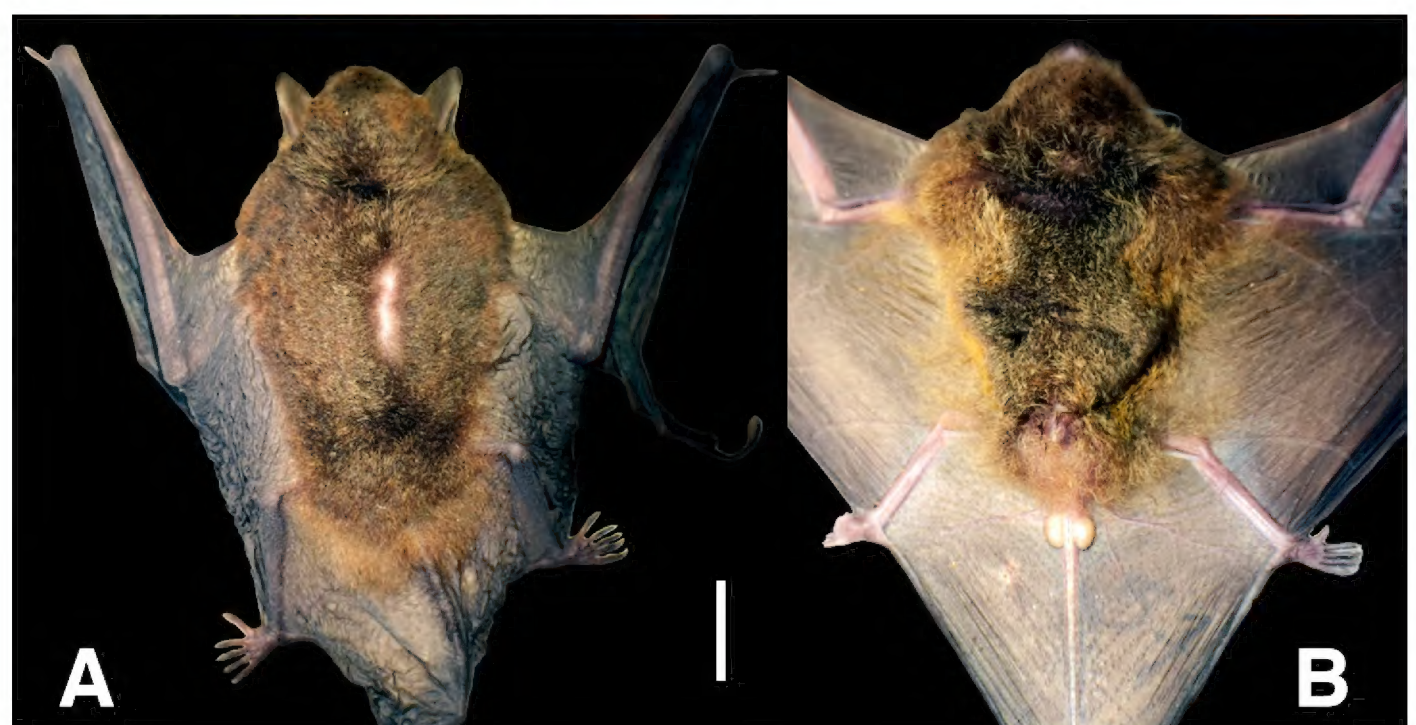
**Figure 3.** Dorsal, ventral, and lateral views of the skull, and lateral view of the mandible of *Myotis moratellii* (MECN 8004). Scale bar = 5 mm. Photos by Jorge Brito.
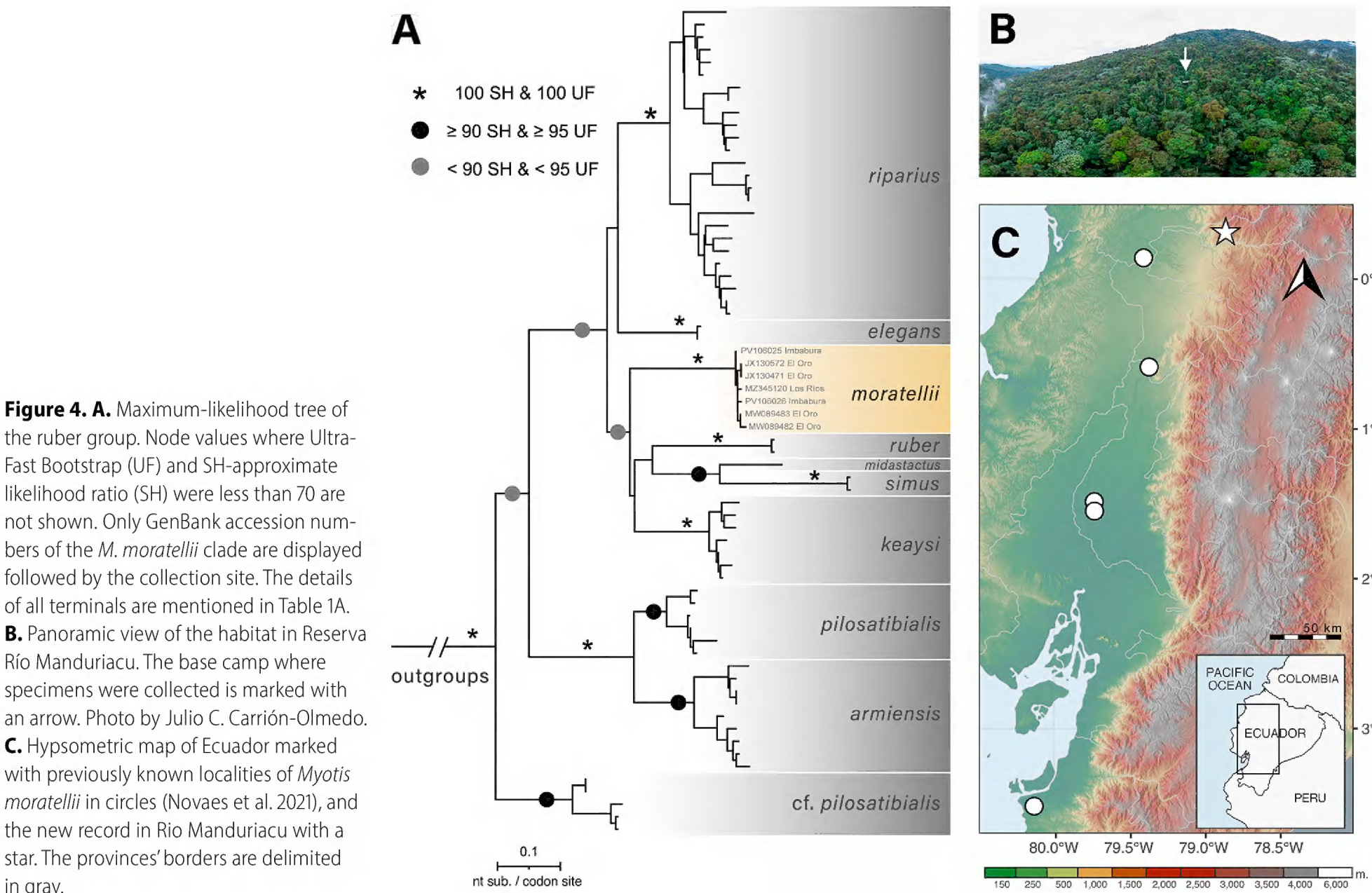
**Table 1.** Summary of measurement comparisons between the specimens collected in this study and *M. moratellii* representatives described in-text and Table 4 in Novaes et al. (2021). Asterisks highlight larger measurements in the Río Manduriacu specimens. Cranial measurements were taken in MECN 8004.

| Measurements (in mm) | This study (*n* = 2) | Novaes et al. 2021 (*n* = 5–6) |
|---|---|---|
| Total length | 77/81.5 | 76–89 |
| Forearm length* | 40/40.2 | 36.4 (35.0–38.2) |
| Tail length | 31/31.5 | 32–38 |
| Ear length | 11.5/12.5 | 12.0 (11.5–13.0) |
| Length of dorsal fur | 6/7 | 6.5 (5.0–7.5) |
| Length of ventral fur* | 5/6 | 4.5 (4.0–5.5) |
| Body weight in grams | 5.5/7.5 | 5–7 |
| Greatest length of skull | 13.7 | 13.89 (13.79–14.05) |
| Condylo-canine length* | 12.7 | 12.35 (12.18–12.55) |
| Condylo-basal length | 13.2 | 13.02 (12.82–13.28) |
| Condylo-incisive length | 13.9 | 13.89 (13.79–14.05) |
| Basal length* | 12.4 | 11.89 (11.71–12.15) |
| Zygomatic breadth | — | 9.04 (8.99–9.14) |
| Mastoid breadth | 7.2 | 7.27 (7.15–7.36) |
| Braincase breadth | 6.5 | 6.61 (4.81–6.48) |
| Postorbital breadth | 3.5 | 3.55 (3.49–3.63) |
| Interorbital breadth | 3.7 | 4.77 (4.60–5.15) |
| Breadth across canines* | 4.0 | 3.86 (3.78–3.90) |
| Breadth across molars* | 5.9 | 5.63 (5.51–5.79) |
| Maxillary toothrow length* | 5.4 | 5.25 (5.16–5.36) |
| Molariform toothrow length* | 3.4 | 3.04 (2.96–3.12) |
| Mandibular length* | 10.9 | 10.22 (10.06–10.42) |
| Mandibular toothrow length | 5.6 | 5.63 (5.54–5.70) |

UF = 100 and SH = 100). The *M. moratellii* clade was recovered as a sister lineage to *M. ruber* + *M. midastactus* + *M. simus* + *M. keaysi* with medium support (Figure 4A; UF = 88.9 and SH = 89). Lastly, the genetic distance of the Río Manduriacu specimens (PV106025, PV106026) to their conspecifics was 0.4%, whereas interspecific divergence values were greater than 11% (Table 2).

**Natural history.** The Reserva Río Manduriacu (Figure 4B) is a 9.66 km$^2$ protected area located in the Chocó ecoregion and the headwaters of the Río Manduriacu, in the western foothills of the Cordillera de los Andes (Albuja et al. 2012; Ron 2020), with altitudes ranging from 1,000 to 1,800 m a.s.l. The habitat is characterized by abundant palms and trees of the families Mimosaceae, Fabaceae, and Burseraceae. The forest canopy reaches 35 m or more, and the trees are covered by mosses, orchids, bromeliads, and ferns. Other bat species

**Figure 4. A.** Maximum-likelihood tree of the ruber group. Node values where Ultra-Fast Bootstrap (UF) and SH-approximate likelihood ratio (SH) were less than 70 are not shown. Only GenBank accession numbers of the *M. moratellii* clade are displayed followed by the collection site. The details of all terminals are mentioned in Table 1A. **B.** Panoramic view of the habitat in Reserva Río Manduriacu. The base camp where specimens were collected is marked with an arrow. Photo by Julio C. Carrión-Olmedo. **C.** Hypsometric map of Ecuador marked with previously known localities of *Myotis moratellii* in circles (Novaes et al. 2021), and the new record in Rio Manduriacu with a star. The provinces' borders are delimited in gray.

found in sympatry with *M. moratellii* were *M. riparius* Handley, 1960, *Anoura cultrata* Handleyi, 1960, *Sturnira bogotensis* Shamel, 1927, *S. ludovici* Anthony, 1924, *S. koopmanhilli* McCarthy, Albuja & Alberico, 2006, *Platyrrhinus dorsalis* Thomas, 1900, and *Lophostoma occidentale* Davis & Carter, 1978.

## DISCUSSION

The new records of *Myotis moratellii* in the Reserva Río Manduriacu (Imbabura Province), represent the tenth documented locality of the species in Ecuador and the first report in the foothill rainforest of the Chocó ecoregion, approximately 63 km away from the most northern site reported previously (Figure 4C). More importantly, it extends the altitudinal range from 150 to 1,240 m a.s.l., making it the highest altitudinal record for *M. moratellii* and with the greatest impact on the ecological knowledge of the species.

The specimens inhabiting this region have darker fur with Ochraceous-Orange and Maize Yellow patches of fur randomly dispersed through the body, in contrast to the lighter specimens reported by Novaes

**Table 2.** Genetic distances of ten species of the ruber group calculated with the Kimura 2-parameter model are shown as percentages. Within-group values are bolded and in the diagonal of the matrix. The asterisk marks specimens MECN 8004 and MECN 8096.

|                          | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    | 10  | 11  |
|--------------------------|------|------|------|------|------|------|------|------|------|-----|-----|
| **1. *M. armiensis***    | **2.6** |      |      |      |      |      |      |      |      |     |     |
| **2. *M.* cf. *pilosatibialis*** | 16.3 | **2.3** |      |      |      |      |      |      |      |     |     |
| **3. *M. elegans***      | 19.6 | 16.2 | **0.2** |      |      |      |      |      |      |     |     |
| **4. *M. keaysi***       | 20.4 | 19.5 | 11.9 | **1.9** |      |      |      |      |      |     |     |
| **5. *M. midastactus***  | 21.8 | 22.6 | 13.8 | 14.2 | —    |      |      |      |      |     |     |
| **6. *M. moratellii****  | 20.7 | 18.1 | 12.0 | 11.8 | 14.4 | **0.3** |      |      |      |     |     |
| **7. *M. moratellii***   | 21.6 | 17.8 | 11.2 | 12.1 | 13.6 | 0.4  | **0.7** |      |      |     |     |
| **8. *M. pilosatibialis*** | 8.7  | 15.3 | 18.4 | 20.1 | 22.5 | 16.1 | 16.3 | **2.0** |      |     |     |
| **9. *M. riparius***     | 23.1 | 19.8 | 10.9 | 15.4 | 15.7 | 13.4 | 13.4 | 19.2 | **5.5** |     |     |
| **10. *M. ruber***       | 25.7 | 20   | 15.6 | 14.4 | 14.8 | 14.5 | 14.0 | 21.4 | 16.9 | **0.3** |     |
| **11. *M. simus***       | 23.1 | 23.6 | 16.5 | 17.1 | 10.3 | 18.1 | 17.3 | 22.3 | 17.5 | 18.5 | **0.3** |

et al. (2021), although the high support of the clade, and genetic distances less than 1%, suggest they are a single evolutionary lineage (Figure 4A, Table 2). The intraspecific differences of pelage color remain poorly explored and understood in bats (Davis and Castleberry 2010). Nevertheless, in the Neotropics, dark and light fur coloration in *Myotis lavali* Moratelli et al., 2011 and *M. nigricans* Schinz, 1821 have been hypothesized to be associated with habitat differences (Moratelli and Wilson 2013).

In fact, the Reserva Río Manduriacu is characterized by a humid cloud forest (Figure 4B), while the specimens reported by Novaes et al. (2021) inhabit seasonal and broadleaf dry forests. Selective pressures in contrasting environments may, therefore, cause a shift in camouflage strategy leading to different coloration patterns (Caro 2005; Caro and Mallarino 2020). However, the numerous biological, ecological, and genetic factors causing these differences are still to be determined.

Finally, *M. moratellii* is known from a small number of museum specimens (Novaes et al. 2021; this study), which could lead us to consider it as a rare species. However, this perceived rarity, could be due to the lack of adequate field studies (Nivelo-Villavicencio et al. 2023) and the intricacy of its morphological identification. Knowledge of the natural history, ecology, and biogeography of the species is essential to design adequate conservation strategies (IUCN 2012), especially in an endangered and fragile ecosystem such as the Chocó (Roy et al. 2018). This note and other studies (Carrión-Bonilla et al. 2024; Korstian et al. 2024) exemplify and underscore the importance of increasing collections in poorly sampled geographic areas, sample sharing, collaborative efforts, and integrating new technologies and traditional approaches to untangle the yet to be discovered cryptic diversity within the genus.

## ADDITIONAL INFORMATION

### Conflict of interest
The authors declare that no competing interests exist.

### Ethical statement
No ethical statement is reported.

### Author contributions
Conceptualization: FXC, JB. Data curation: FXC, LS, JB. Formal analysis: FXC, JB. Funding acquisition: FXC, JB. Investigation: FXC, JB. Methodology: FXC, JB. Supervision: FXC, JB. Writing – original draft: FXC, JB. Writing – review and editing: FXC, LS, JB.

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### Data availability
All data that supports the findings of this study are available in the main text and Appendix Table 1A.

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## APPENDIX

**Table 1A.** *Myotis* specimens of the ruber group used in phylogenetics analyses. Species names correspond to the latest revision of Carrión-Bonilla and Cook (2020), Novaes et al. (2021), and Carrión-Bonilla et al. (2024). Acronyms of museums correspond to **ALP**: Federal Rural University of Rio de Janeiro, Seropédica, Brazil; **AMNH**: American Museum of Natural History; **CM**: Carnegie Museum of Natural History, Pittsburg, USA; **JAG**: Jane A. Groen; **MECN**: División de Mastozoología, Instituto Nacional de Biodiversidad, Quito, Ecuador; **MSB**: Museum of Southwestern Biology, Division of Mammals, The University of New Mexico; **MVZ**: Museum of Vertebrate Zoology, Mammal Collection, University of California Berkeley; **QCAZ**: Museo de Zoología, División de Mamíferos, Pontificia Universidad Católica del Ecuador; **SM**: Sumiko Matsumura; **SMF**: Senckenberg Museum of Frankfurt, Mammalogy Collection; **SNOMNH**: Sam Noble Oklahoma Museum of Natural History; **TTU** and **TK**: Natural Science Research Laboratory Mammal Collection at Texas Tech University; **USNM**: Smithsonian National Museum of Natural History.

| Species | GenBank # | Voucher # | Source |
|---|---|---|---|
| *M. armiensis* | JX130435 | TK 22503 | Larsen et al. 2012 |
| *M. armiensis* | JX130514 | TK 104288 | Larsen et al. 2012 |
| *M. armiensis* | MW025265 | MSB MAMM 262089 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MW025266 | MSB MAMM 262237 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MW025267 | MSB MAMM 262788 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MW025268 | MSB MAMM 262085 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MW025269 | QCAZ M 17245 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MW025274 | QCAZ M 12461 | Carrión-Bonilla and Cook 2020 |
| *M. armiensis* | MZ345121 | USNM MAMM 370890 | Novaes et al. 2021 |
| *M.* cf. *pilosatibialis* | JX130449 | TK 13526 | Larsen et al. 2012 |
| *M.* cf. *pilosatibialis* | JX130489 | CM 55764 | Larsen et al. 2012 |
| *M.* cf. *pilosatibialis* | JX130525 | JAG 286 | Larsen et al. 2012 |

| Species | GenBank # | Voucher # | Source |
|---|---|---|---|
| *M.* cf. *pilosatibialis* | MF143477 | TK 13525 | Platt et al. 2018 |
| *M.* cf. *pilosatibialis* | MW025270 | MVZ MAMM 226977 | Carrión-Bonilla and Cook 2020 |
| *M. elegans* | JX130479 | TK 101723 | Larsen et al. 2012 |
| *M. elegans* | JX130480 | TK 101479 | Larsen et al. 2012 |
| *M. keaysi* | JX130516 | QCAZ 11380 | Larsen et al. 2012 |
| *M. keaysi* | JX130517 | QCAZ 11383 | Larsen et al. 2012 |
| *M. keaysi* | MW025273 | MSB 70381 | Carrión-Bonilla and Cook 2020 |
| *M. keaysi* | MW089478 | QCAZ MAMM12039 | Carrión-Bonilla et al. 2024 |
| *M. keaysi* | MW089479 | QCAZ MAMM12038 | Carrión-Bonilla et al. 2024 |
| *M. keaysi* | MW089480 | SNOMNH MAMM23783 | Carrión-Bonilla et al. 2024 |
| *M. keaysi* | MW089481 | AMNH MAMM268651 | Carrión-Bonilla et al. 2024 |
| *M. midastactus* | MW323450 | USNM MAMM 584502 | Novaes et al. 2021 |
| *M. moratellii* | JX130571 | TK 135095 | Larsen et al. 2012 |
| *M. moratellii* | JX130572 | TK 135069 | Larsen et al. 2012 |
| *M. moratellii* | MW089482 | QCAZ MAMM9159 | Carrión-Bonilla et al. 2024 |
| *M. moratellii* | MW089483 | QCAZ MAMM9623 | Carrión-Bonilla et al. 2024 |
| *M. moratellii* | MZ345120 | USNM MAMM 513482 | Novaes et al. 2021 |
| *M. moratellii* | PV106025 | MECN 8004 | This study |
| *M. moratellii* | PV106026 | MECN 8096 | This study |
| *M. pilosatibialis* | JX130518 | TK 14521 | Larsen et al. 2012 |
| *M. pilosatibialis* | JX130519 | TK 34869 | Larsen et al. 2012 |
| *M. pilosatibialis* | JX130526 | TK 14520 | Larsen et al. 2012 |
| *M. pilosatibialis* | MW025271 | MVZ MAMM 226976 | Carrión-Bonilla and Cook 2020 |
| *M. pilosatibialis* | MW025272 | MVZ MAMM 226973 | Carrión-Bonilla and Cook 2020 |
| *M. pilosatibialis* | MW025275 | MVZ 224798 | Carrión-Bonilla and Cook 2020 |
| *M. riparius* | AF376866 | MVZ 185996 | Ruedi and Mayer 2001 |
| *M. riparius* | AM261891 | No voucher | Stadelmann et al. 2007 |
| *M. riparius* | JX130436 | TK 22703 | Larsen et al. 2012 |
| *M. riparius* | JX130469 | TK 104572 | Larsen et al. 2012 |
| *M. riparius* | JX130473 | CM 68443 | Larsen et al. 2012 |
| *M. riparius* | JX130474 | CM 78659 | Larsen et al. 2012 |
| *M. riparius* | JX130485 | TK 63827 | Larsen et al. 2012 |
| *M. riparius* | JX130486 | TK 56784 | Larsen et al. 2012 |
| *M. riparius* | JX130488 | TK 121165 | Larsen et al. 2012 |
| *M. riparius* | JX130490 | CM 78651 | Larsen et al. 2012 |
| *M. riparius* | JX130491 | TK 63402 | Larsen et al. 2012 |
| *M. riparius* | JX130492 | TK 135564 | Larsen et al. 2012 |
| *M. riparius* | JX130506 | TK 104318 | Larsen et al. 2012 |
| *M. riparius* | JX130513 | TK 104098 | Larsen et al. 2012 |
| *M. riparius* | JX130515 | TK 104573 | Larsen et al. 2012 |
| *M. riparius* | MW089486 | QCAZ MAMM9165 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089488 | QCAZ MAMM13894 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089490 | QCAZ MAMM15339 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089492 | QCAZ MAMM13936 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089493 | SNOMNH MAMM36220 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089494 | AMNH MAMM261808 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW089495 | MSB MAMM70383 | Carrión-Bonilla et al. 2024 |
| *M. riparius* | MW323447 | ALP 10926 | Novaes et al. 2021 |
| *M. riparius* | MW323448 | ALP 10927 | Novaes et al. 2021 |
| *M. riparius* | MW323449 | ALP 11024 | Novaes et al. 2021 |
| *M. ruber* | AF376867 | MVZ 185999 | Ruedi and Mayer 2001 |
| *M. ruber* | MF143478 | MVZ 185692 | Platt et al. 2018 |
| *M. simus* | JX130481 | TTU 46348 | Larsen et al. 2012 |
| *M. simus* | MF143473 | TK 22688 | Platt et al. 2018 |
| **Outgroups** | | | |
| *M.* cf. *nigricans* | JX130496 | TK 64475 | Larsen et al. 2012 |
| *M. lavali* | AF376864 | MVZ-M 185682 | Ruedi and Mayer 2001 |
| *M. levis* | JX130475 | TK 49150 | Ruedi and Mayer 2001 |